

SCORE Search Results Details for Application 10623500 and Search Result us-10-623-500-1.rge.

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This page gives you Search Results detail for the Application 10623500 and Search Result us-10-623-500-1.rge.
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2006, 13:07:01 ; Search time 2103.59 Seconds
(without alignments)
10214.354 Million cell updates/sec

Title: US-10-623-500-1
Perfect score: 378
Sequence: 1 tactacagataacacgacag.....atccaccgatccatggcatg 378

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	378	100.0	378	6	CQ774396	CQ774396 Sequence
2	378	100.0	1236	6	CQ774397	CQ774397 Sequence
c 3	376	99.5	8514	6	CQ774407	CQ774407 Sequence
4	361	95.5	2136	6	CS077377	CS077377 Sequence
5	359.4	95.1	3583	6	CS077378	CS077378 Sequence
6	62.8	16.6	604	6	CQ774410	CQ774410 Sequence
c 7	62.8	16.6	8692	6	CQ774408	CQ774408 Sequence
c 8	38.4	10.2	174626	9	AC125021	AC125021 Mus muscu
c 9	38.4	10.2	189884	9	AC125017	AC125017 Mus muscu
10	37.8	10.0	110000	14	CT005266_06	Continuation (7 of
11	37.8	10.0	110000	14	CT005266_07	Continuation (8 of
c 12	37.8	10.0	134866	9	AL844206	AL844206 Mouse DNA
c 13	37.4	9.9	166194	14	AC139647	AC139647 Rattus no
14	37.4	9.9	230661	14	AC132770	AC132770 Rattus no
15	36.8	9.7	228193	14	AC095493	AC095493 Rattus no
16	36.8	9.7	245229	14	AC131126	AC131126 Rattus no
17	36.6	9.7	35880	9	AY226577	AY226577 Mus muscu
18	36.6	9.7	196249	9	AC092202	AC092202 Mus muscu
c 19	35.4	9.4	110000	15	AP008210_028	Continuation (29 o
20	35.4	9.4	122697	14	AC165945	AC165945 Mus muscu
21	35.4	9.4	169452	9	AL772237	AL772237 Mouse DNA
c 22	35.4	9.4	182079	14	OSJN00133	AL662943 Oryza sat
23	35.4	9.4	204091	14	AC152442	AC152442 Bos tauru
c 24	35.4	9.4	208835	9	AL591952	AL591952 Mouse DNA
25	35	9.3	5959	9	AK129095	AK129095 Mus muscu
c 26	35	9.3	179454	14	AC123737	AC123737 Mus muscu
c 27	35	9.3	181442	9	AC114917	AC114917 Mus muscu
c 28	35	9.3	192065	14	AC149556	AC149556 Papio anu
29	35	9.3	214765	14	AC096238	AC096238 Rattus no
c 30	35	9.3	229413	9	AC151999	AC151999 Mus muscu
31	35	9.3	265537	14	AC087228	AC087228 Mus muscu
c 32	34.8	9.2	125020	8	AF429315	AF429315 Homo sapi
33	34.8	9.2	131184	9	AL844513	AL844513 Mouse DNA
34	34.8	9.2	186895	9	AC115818	AC115818 Mus muscu
35	34.8	9.2	192676	9	AL671706	AL671706 Mouse DNA
c 36	34.8	9.2	199981	9	AC157787	AC157787 Mus muscu
c 37	34.8	9.2	232305	14	AC152577	AC152577 Bos tauru
38	34.8	9.2	234105	9	AC091606	AC091606 Mus Muscu
c 39	34.8	9.2	235328	14	AC094823	AC094823 Rattus no
40	34.8	9.2	244471	14	AC106677	AC106677 Rattus no
41	34.8	9.2	305128	1	AE017203	AE017203 Lactobaci
42	34.8	9.2	349980	6	AX926715	AX926715 Sequence
c 43	34.6	9.2	171323	9	AC156394	AC156394 Mus muscu
c 44	34.4	9.1	79379	9	AL591486	AL591486 Mouse DNA
c 45	34.4	9.1	97255	8	AL590482	AL590482 Human DNA

ALIGNMENTS

RESULT 1

CQ774396

LOCUS CQ774396 378 bp DNA linear PAT 06-MAR-2004

DEFINITION Sequence 1 from Patent WO2004013169.

ACCESSION CQ774396

VERSION CQ774396.1 GI:45237632

SCORE Search Results Details for Application 106 us-10-623-500-1.rng.

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OM nucleic - nucleic search, using sw model

Run on: April 28, 2006, 12:45:12 ; Search time 235.606 Seconds
(without alignments)
10692.658 Million cell updates/sec

Title: US-10-623-500-1
Perfect score: 378
Sequence: 1 tactacagataacacgacag.....atccaccgatccatggcatg 378

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query		Length	DB	ID	Description	
	No.	Score Match					
c	1	378	100.0	378	12	ADK70969	Adk70969 Corn root
	2	378	100.0	1236	12	ADK70970	Adk70970 Corn root
	3	376	99.5	8514	12	ADK70980	Adk70980 Nucleotid
	4	361	95.5	2136	14	ADZ67283	Adz67283 Maize pro
	5	359.4	95.1	3583	14	ADZ67284	Adz67284 Maize pro
c	6	62.8	16.6	604	12	ADK70983	Adk70983 Corn root
	7	62.8	16.6	8692	12	ADK70981	Adk70981 Nucleotid
	8	34.8	9.2	110000	10	ADF77343_13	Continuation (14 o
	9	34.8	9.2	110000	10	ADF77343_14	Continuation (15 o
	10	34	9.0	1667	13	ADT16263	Adt16263 Plant cDN
c	11	33.6	8.9	2000	8	ADA71938	Ada71938 Rice gene
	12	33.2	8.8	458	5	ADL44264	Adl44264 Human ova
	13	33	8.7	2940	13	ADO83893	Ado83893 Plant ful
	14	32.8	8.7	110000	3	AAF22305_01	Continuation (2 of
	15	32.6	8.6	405	12	ADP93916	Adp93916 Cotton ex
c	16	32.6	8.6	4409	4	ABL28408	Abl28408 Drosophil
c	17	31.8	8.4	3111	13	ADS60875	Ads60875 Bacterial
c	18	31.8	8.4	12537	2	AAT41705	Aat41705 Lymphocyt
c	19	31.8	8.4	15755	12	ADM66947	Adm66947 Murine ad
c	20	31.6	8.4	479	5	ADI72901	Adi72901 Human ova
c	21	31.6	8.4	479	5	ADL38039	Adl38039 Human ova
c	22	31.6	8.4	599	5	ADL44423	Adl44423 Human ova
	23	31.6	8.4	5082	6	ABQ70953	Abq70953 Listeria
c	24	31.6	8.4	42203	13	ABD32583	Abd32583 Mouse can
	25	31.6	8.4	110000	6	ABA03041_22	Continuation (23 o
	26	31.6	8.4	122859	11	ACN43872	Acn43872 Mouse gen
c	27	31.6	8.4	304326	13	ADS15253	Ads15253 Rat senso
	28	31.4	8.3	110000	14	AEB42736_6	Continuation (7 of
	29	31.4	8.3	148497	12	ADQ18925	Adq18925 Human sof
c	30	31.4	8.3	207461	14	AEB39170	Aeb39170 L. pneumo
c	31	31.4	8.3	243335	14	AEB42735	Aeb42735 L. pneumo
c	32	31.4	8.3	298667	14	AEB39173	Aeb39173 L. pneumo
	33	31.2	8.3	1062	3	AAF16268	Aaf16268 Human pro
	34	31.2	8.3	1449	13	ADS58811	Ads58811 Bacterial
	35	31.2	8.3	3003	4	AAK52700	Aak52700 Human pol
	36	31.2	8.3	3003	4	AAK52699	Aak52699 Human pol
	37	31.2	8.3	3003	4	AAK52701	Aak52701 Human pol
	38	31.2	8.3	4238	6	ABL69127	Abl69127 Kidney ca
	39	31.2	8.3	4238	6	ABK84776	Abk84776 Human cDN
	40	31.2	8.3	4238	10	ADG32944	Adg32944 Human DNA
	41	31.2	8.3	4238	11	ADI32121	Adi32121 Human cDN
	42	31.2	8.3	4238	12	ADQ19339	Adq19339 Human sof
	43	31.2	8.3	4238	12	ADQ85464	Adq85464 Human tum
	44	31.2	8.3	4238	13	ADS84188	Ads84188 Human lym
	45	31.2	8.3	4238	14	ADX05619	Adx05619 Cyclin-de

ALIGNMENTS

RESULT 1

ADK70969

ID ADK70969 standard; DNA; 378 BP.

XX

AC ADK70969;

XX

DT 06-MAY-2004 (first entry)

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OM nucleic - nucleic search, using sw model

Run on: April 28, 2006, 12:37:49 ; Search time 281.509 Seconds
(without alignments)
2386.842 Million cell updates/sec

Title: US-10-623-500-1
Perfect score: 378
Sequence: 1 tactacagataaacacgacag.....atccaccgatccatggcatg 378

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	%					
No.	Score	Match	Length	DB	ID	Description	

	1	32.2	8.5	525	3	US-09-248-796A-1337	Sequence 1337, Ap
c	2	31.8	8.4	12537	2	US-08-611-280-4	Sequence 4, Appli
c	3	31.8	8.4	12537	3	US-09-195-940-4	Sequence 4, Appli
c	4	31.8	8.4	12537	3	US-09-562-466-4	Sequence 4, Appli
	5	31.2	8.3	4238	3	US-09-023-655-1447	Sequence 1447, Ap
	6	30.8	8.1	264665	3	US-09-949-016-13747	Sequence 13747, A
	7	30.6	8.1	996	3	US-09-270-767-15059	Sequence 15059, A
	8	30.6	8.1	258775	3	US-09-949-016-16435	Sequence 16435, A
	9	30	7.9	601	3	US-09-949-016-126120	Sequence 126120,
	10	30	7.9	1703	3	US-09-662-254B-45	Sequence 45, Appl
c	11	30	7.9	50000	3	US-09-662-254B-25	Sequence 25, Appl
	12	29.8	7.9	440	3	US-09-621-976-17717	Sequence 17717, A
c	13	29.8	7.9	570	3	US-09-248-796A-14078	Sequence 14078, A
	14	29.8	7.9	25370	3	US-09-949-016-12109	Sequence 12109, A
	15	29.8	7.9	25375	3	US-09-949-016-15880	Sequence 15880, A
	16	29.8	7.9	75480	3	US-09-949-016-16090	Sequence 16090, A
c	17	29.6	7.8	1396	3	US-09-311-021-75	Sequence 75, Appl
c	18	29.6	7.8	1608	2	US-08-855-518-2	Sequence 2, Appli
c	19	29.6	7.8	1723	3	US-09-949-016-4838	Sequence 4838, Ap
c	20	29.6	7.8	1904	2	US-08-933-750C-95	Sequence 95, Appl
c	21	29.6	7.8	1904	3	US-09-234-613-95	Sequence 95, Appl
c	22	29.6	7.8	1986	3	US-10-104-047-1331	Sequence 1331, Ap
	23	29.6	7.8	8942	3	US-09-949-016-15194	Sequence 15194, A
c	24	29.6	7.8	23716	3	US-09-949-016-16580	Sequence 16580, A
	25	29.4	7.8	601	3	US-09-949-016-126119	Sequence 126119,
	26	29.4	7.8	601	3	US-09-949-016-135257	Sequence 135257,
	27	29.4	7.8	28494	3	US-09-949-016-13200	Sequence 13200, A
	28	29.4	7.8	35007	3	US-09-949-016-15330	Sequence 15330, A
	29	29.4	7.8	107421	3	US-09-949-016-15532	Sequence 15532, A
c	30	29.2	7.7	677	3	US-09-270-767-2758	Sequence 2758, Ap
c	31	29.2	7.7	677	3	US-09-270-767-18040	Sequence 18040, A
c	32	29.2	7.7	100550	3	US-09-949-016-11835	Sequence 11835, A
c	33	29.2	7.7	100551	3	US-09-949-016-16207	Sequence 16207, A
c	34	29	7.7	3591	3	US-10-237-551-191	Sequence 191, App
c	35	29	7.7	3591	3	US-10-237-551-221	Sequence 221, App
	36	29	7.7	28770	3	US-09-817-198C-3	Sequence 3, Appli
c	37	29	7.7	52496	3	US-09-949-016-16118	Sequence 16118, A
c	38	29	7.7	52496	3	US-09-949-016-16119	Sequence 16119, A
	39	29	7.7	154746	3	US-09-827-688-8	Sequence 8, Appli
c	40	29	7.7	194790	3	US-09-949-016-15393	Sequence 15393, A
c	41	28.8	7.6	274	3	US-09-313-294A-544	Sequence 544, App
	42	28.8	7.6	1773	3	US-09-194-949A-14	Sequence 14, Appl
	43	28.8	7.6	7122	3	US-09-318-448-2	Sequence 2, Appli
	44	28.8	7.6	7122	3	US-09-347-878-4	Sequence 4, Appli
	45	28.8	7.6	7122	3	US-09-577-266-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-248-796A-1337

; Sequence 1337, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

SCORE Search Results Details for Application 10623500 and Search Result us-10-623-500-1.rnpbm.

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OM nucleic - nucleic search, using sw model

Run on: April 28, 2006, 13:38:42 ; Search time 351.77 Seconds
(without alignments)
8886.003 Million cell updates/sec

Title: US-10-623-500-1
Perfect score: 378
Sequence: 1 tactacagataacacgacag.....atccaccgatccatggcatg 378

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	378	100.0	378	7	US-10-623-500-1	Sequence 1, Appli
2	378	100.0	1236	7	US-10-623-500-2	Sequence 2, Appli
c 3	376	99.5	8514	7	US-10-623-500-12	Sequence 12, Appl
4	361	95.5	2136	9	US-10-961-629-1	Sequence 1, Appli
5	359.4	95.1	3583	9	US-10-961-629-2	Sequence 2, Appli
6	62.8	16.6	604	7	US-10-623-500-15	Sequence 15, Appl
c 7	62.8	16.6	8692	7	US-10-623-500-13	Sequence 13, Appl
c 8	35.4	9.4	3699	7	US-10-437-963-20415	Sequence 20415, A
c 9	34.2	9.0	602	4	US-09-925-065A-56902	Sequence 56902, A
10	34	9.0	1667	8	US-10-739-930-1589	Sequence 1589, Ap
c 11	33.2	8.8	458	3	US-09-814-353-18154	Sequence 18154, A
12	33	8.7	2904	8	US-10-425-115-173235	Sequence 173235,
13	33	8.7	2940	7	US-10-425-114-2613	Sequence 2613, Ap
14	32.8	8.7	653	4	US-09-925-065A-528523	Sequence 528523,
15	32.8	8.7	670	7	US-10-767-701-7934	Sequence 7934, Ap
16	32.8	8.7	676	7	US-10-767-701-7933	Sequence 7933, Ap
c 17	32.6	8.6	405	3	US-09-732-627A-2927	Sequence 2927, Ap
18	32.6	8.6	598	4	US-09-925-065A-794856	Sequence 794856,
19	32.6	8.6	598	4	US-09-925-065A-850557	Sequence 850557,
c 20	32.6	8.6	4409	10	US-11-097-143-39853	Sequence 39853, A
21	32.4	8.6	625	4	US-09-925-065A-519273	Sequence 519273,
c 22	32	8.5	347	3	US-09-783-590-2002	Sequence 2002, Ap
23	32	8.5	1747	7	US-10-424-599-30555	Sequence 30555, A
c 24	31.8	8.4	3111	6	US-10-369-493-36549	Sequence 36549, A
c 25	31.6	8.4	479	3	US-09-814-353-5643	Sequence 5643, Ap
c 26	31.6	8.4	479	3	US-09-814-353-11929	Sequence 11929, A
c 27	31.6	8.4	508	4	US-09-925-065A-839422	Sequence 839422,
28	31.6	8.4	517	4	US-09-925-065A-829705	Sequence 829705,
c 29	31.6	8.4	599	3	US-09-814-353-18313	Sequence 18313, A
c 30	31.6	8.4	624	4	US-09-925-065A-211033	Sequence 211033,
c 31	31.6	8.4	624	4	US-09-925-065A-211034	Sequence 211034,
32	31.6	8.4	658	5	US-10-027-632-188129	Sequence 188129,
33	31.6	8.4	658	6	US-10-027-632-188129	Sequence 188129,
34	31.6	8.4	1670	4	US-09-925-065A-554931	Sequence 554931,
35	31.6	8.4	5082	7	US-10-398-221-3766	Sequence 3766, Ap
c 36	31.6	8.4	42203	7	US-10-367-094-53	Sequence 53, Appl
37	31.6	8.4	122859	5	US-10-087-192-37	Sequence 37, Appl
38	31.4	8.3	453	7	US-10-767-701-25614	Sequence 25614, A
39	31.4	8.3	459	5	US-10-027-632-1705	Sequence 1705, Ap
40	31.4	8.3	459	6	US-10-027-632-1705	Sequence 1705, Ap
41	31.4	8.3	148497	8	US-10-723-860-1744	Sequence 1744, Ap
42	31.4	8.3	148497	9	US-10-756-149-675	Sequence 675, App
c 43	31.2	8.3	508	4	US-09-925-065A-839421	Sequence 839421,
44	31.2	8.3	517	4	US-09-925-065A-829706	Sequence 829706,
45	31.2	8.3	590	4	US-09-925-065A-737930	Sequence 737930,

ALIGNMENTS

RESULT 1

US-10-623-500-1

; Sequence 1, Application US/10623500

; Publication No. US20040133945A1

; GENERAL INFORMATION:

; APPLICANT: Bayer BioScience N.V.

; APPLICANT: Greet, Vanderkimpen

SCORE Search Results Details for Application 10623500 and Search Result us-10-623-500-1.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on: April 28, 2006, 14:15:53 ; Search time 278.465 Seconds
(without alignments)
5512.943 Million cell updates/sec

Title: US-10-623-500-1
Perfect score: 378
Sequence: 1 tactacagataacacgacag.....atccaccgatccatggcatg 378

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9295968 seqs, 2030634719 residues

Total number of hits satisfying chosen parameters: 18591936

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*

- 1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 2: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /SIDS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 5: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 6: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
- 7: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 8: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
- 9: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
- 10: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq3:*
- 11: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 12: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
- 13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
- 14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
- 15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
c 1	34.2	9.0	602	6	US-09-925-065A-56902	Sequence 56902, A
c 2	34.2	9.0	602	9	US-10-301-480-158140	Sequence 158140,
c 3	34.2	9.0	602	10	US-10-301-480-771549	Sequence 771549,
c 4	33	8.7	1227	14	US-11-136-527-1590	Sequence 1590, Ap
5	32.8	8.7	653	6	US-09-925-065A-528523	Sequence 528523,
c 6	32.8	8.7	1082144	14	US-11-117-187-211	Sequence 211, App
7	32.6	8.6	598	6	US-09-925-065A-794856	Sequence 794856,
8	32.6	8.6	598	6	US-09-925-065A-850557	Sequence 850557,
9	32.4	8.6	625	6	US-09-925-065A-519273	Sequence 519273,
10	32.2	8.5	1757	14	US-11-136-527-2405	Sequence 2405, Ap
c 11	31.6	8.4	508	6	US-09-925-065A-839422	Sequence 839422,
12	31.6	8.4	517	6	US-09-925-065A-829705	Sequence 829705,
c 13	31.6	8.4	624	6	US-09-925-065A-211033	Sequence 211033,
c 14	31.6	8.4	624	6	US-09-925-065A-211034	Sequence 211034,
c 15	31.6	8.4	634	10	US-10-301-480-298282	Sequence 298282,
c 16	31.6	8.4	634	10	US-10-301-480-298283	Sequence 298283,
c 17	31.6	8.4	634	10	US-10-301-480-911691	Sequence 911691,
c 18	31.6	8.4	634	10	US-10-301-480-911692	Sequence 911692,
19	31.6	8.4	1670	6	US-09-925-065A-554931	Sequence 554931,
20	31.6	8.4	2944528	11	US-11-045-004-1	Sequence 1, Appli
21	31.4	8.3	998	10	US-10-301-480-542470	Sequence 542470,
22	31.4	8.3	998	10	US-10-301-480-1155879	Sequence 1155879,
23	31.4	8.3	1481	8	US-10-750-185-48717	Sequence 48717, A
24	31.4	8.3	1481	8	US-10-750-623-48717	Sequence 48717, A
c 25	31.2	8.3	508	6	US-09-925-065A-839421	Sequence 839421,
26	31.2	8.3	517	6	US-09-925-065A-829706	Sequence 829706,
27	31.2	8.3	590	6	US-09-925-065A-737930	Sequence 737930,
28	31.2	8.3	590	6	US-09-925-065A-814947	Sequence 814947,
29	31.2	8.3	4238	14	US-11-000-688-368	Sequence 368, App
c 30	31.2	8.3	228006	9	US-10-330-773-119	Sequence 119, App
c 31	31	8.2	489	6	US-09-925-065A-135565	Sequence 135565,
c 32	31	8.2	493	10	US-10-301-480-231186	Sequence 231186,
c 33	31	8.2	493	10	US-10-301-480-844595	Sequence 844595,
c 34	31	8.2	709	10	US-10-301-480-576204	Sequence 576204,
c 35	31	8.2	709	10	US-10-301-480-1189613	Sequence 1189613,
36	31	8.2	1349	6	US-09-925-065A-554808	Sequence 554808,
37	31	8.2	1349	6	US-09-925-065A-554809	Sequence 554809,
38	31	8.2	193363	14	US-11-112-908-32	Sequence 32, Appl
39	30.8	8.1	605	6	US-09-925-065A-693394	Sequence 693394,
40	30.6	8.1	631	10	US-10-301-480-278919	Sequence 278919,
41	30.6	8.1	631	10	US-10-301-480-892328	Sequence 892328,
42	30.6	8.1	634	6	US-09-925-065A-189049	Sequence 189049,
43	30.6	8.1	642	10	US-10-301-480-538430	Sequence 538430,
44	30.6	8.1	642	10	US-10-301-480-1151839	Sequence 1151839,
45	30.6	8.1	1134	6	US-09-925-065A-39663	Sequence 39663, A

ALIGNMENTS

RESULT 1

US-09-925-065A-56902/c